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(54) Title: THROMBIN RECEPTOR HOMOLOG		
(57) Abstract		
<p>The present invention provides nucleotide and amino acid sequences that identify and encode a novel thrombin receptor homolog (TRH) expressed in human liver. The present invention also provides for antisense molecules to the nucleotide sequences which encode TRH, diagnostic tests based on TRH encoding nucleic acid molecules, expression vectors for the production of purified TRH, antibodies capable of binding to TRH, hybridization probes or oligonucleotides for the detection of TRH-encoding nucleotide sequences, genetically engineered host cells for the expression of TRH, and antagonists, antibodies and inhibitors which bind to the polypeptide TRH.</p>		

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THROMBIN RECEPTOR HOMOLOG

TECHNICAL FIELD

The present invention is in the field of molecular biology; more particularly, the present invention describes the nucleic acid and amino acid sequences of a thrombin receptor homolog.

BACKGROUND ART

The thrombin receptor is a G-protein coupled seven transmembrane receptor (T7G) which is present on platelets, endothelial cells, fibroblasts, mesangial cells, neural cells and smooth muscle cells. This receptor is activated by the irreversible cleavage of the extracellular, amino terminal sequence between arg⁴¹ and ser⁴² by thrombin or another serine protease. In normal endothelial cells, activation of the thrombin receptor stimulates intracellular Gq-protein mediated phosphoinositide metabolism and Gi-protein mediated adenylate cyclase inhibition. Additionally, endothelial cells secrete endothelin-derived relaxing factor (EDRF). Subsequently EDRF stimulates soluble guanylate cyclase release followed by formation of cyclic GMP and relaxation of smooth muscle. Another function of EDRF is the inhibition of platelet adhesion and aggregation which is beneficial to blood flow.

Wilcox et al (1994, Circ Res 75:1029-38) disclosed that in rat aorta smooth muscle, thrombin receptor expression increases soon after vascular injury and triggers cell proliferation in the neointima. Blocking the thrombin receptor's cleavage site with antibody halts thrombin-induced cell proliferation. Following cleavage and activation, thrombin receptors become desensitized, and they are internalized for recycling. Receptor recycling and replacement limit the duration of thrombin initiated events.

The thrombin receptor has at least four potential N- glycosylation sites, Asn³⁵, Asn⁶², Asn⁷⁵, and Asn²⁵⁹. The presence of carbohydrate greatly affects the differences in size and predicted mass reported for thrombin receptors. Moreover, glycosylation may account for as much as 30% of the mass of these receptors and apparently determines their distribution (Brass LF et al (1992) J Biol Chem 267:13795-8).

The thrombin receptor is classified with the nonneurokinin T7G receptors which include many glycoprotein hormone receptors such as those for luteinizing hormone (LH) and follicle stimulating hormone (FSH). They have very long N-termini, bind a common ligand structural motif with low affinity to activate the receptor, and rely on the N-termini and extracellular loops to impart high affinity and specificity (Bolander FF (1994) Molecular Endocrinology, Academic Press, San Diego CA).

They are related to other T7Gs by their seven hydrophobic domains which span the plasma membrane and form a bundle of antiparallel helices. These transmembrane segments (TMS) are designated by roman numerals I-VII and account for structural and functional features of the receptor. In most cases, the bundle forms a binding pocket; however, when the binding site must accommodate more bulky molecules, the extracellular N-terminal segment or one or more of the three extracellular loops participate in binding (Watson S and Arkinstall S (1994) The G-Protein Linked Receptor Facts Book, Academic Press, San Diego CA) and in subsequent induction of conformational change in intracellular portions of the receptor. The activated receptor in turn, interacts with an intracellular G-protein complex which mediates further intracellular signalling activities generally the production of second messengers such as cyclic AMP (cAMP), phospholipase C, inositol triphosphate or ion channel proteins.

Thrombin receptor homologs are expressed in tissues such as the liver which is briefly described below.

The basic functional unit of the human liver is the lobule, and each lobule consists of hepatic cellular plates which encircle a central vein. Small bile canaliculi bisect the plates and empty into ducts found in septa between the lobules. Hepatic sinusoids associated with the septa are lined with endothelial and Kupffer cells. Bacteria and organic matter are removed from the portal blood by the Kupffer cells which also express high levels of class II major histocompatibility complex proteins and release nitric oxide, interleukin (IL)-1, IL-6, and TNF.

Although they do not normally produce erythrocytes or divide in adults, liver cells are basically embryonic. If a portion of the liver is destroyed or removed, the remaining parenchyma can regenerate the entire organ. Liver cells are characterized by large amounts of endoplasmic reticulum which is consistent with their metabolic, storage, endo- and exo-cytotic activities. The liver has three main functions: 1) vascular, for the storage and filtration of blood; 2) metabolic, for regulation of glucose and storage of glycogen and fat; and 3) secretory/excretory, for regulation of hormones and degradation of toxic substances.

The normal blood volume of the liver is 450 ml, and an average blood flow through the liver is 1450 ml/min. The liver can store an extra 500-1000 ml of blood or supply extra blood after trauma. Half of the lymph produced in the body comes from the liver via drainage through the spaces of Disse (located below the hepatic cells). High blood pressure within the liver is a significant factor in edema or ascites.

Liver cells have a very high rate of metabolism; and they process, synthesize and degrade carbohydrates, fats and proteins simultaneously. Carbohydrate metabolism consists of storage of glycogen, conversion of fructose and galactose to glucose, and gluconeogenesis. The

liver regulates the amount of glucose in the blood in response to hormones.

Liver cells have special fat-metabolizing functions, the oxidation of fatty acids and the production of lipoproteins, phospholipids and cholesterol. The lipoproteins transport phospholipids and cholesterol to other areas where they are used to form cellular membranes and other substances important in cellular function. Most of the conversion of carbohydrates and proteins to fat occurs in the liver although storage may be in adipose tissue elsewhere in the body. The liver also stores the fat-soluble vitamins and iron.

The liver forms 90% of the plasma proteins, particularly albumin and various globulins, at the rate of 15-50 g/day. The liver also produces haptoglobin, ceruloplasmin, and transferrin in response to cytokines. It manufactures nonessential amino acids; and in the presence of vitamin K, synthesizes accelerator globulin, erythropoietin, and the clotting factors I, II, V, VII, IX and X.

Lipid-soluble drugs are usually detoxified in the liver. Phase I reactions involve enzymatic modification of reactive groups on drug molecules by oxidation, reduction, hydroxylation, sulfoxidation, deamination, dealkylation or methylation. Such modifications deactivate barbiturates and benzodiazepines and activate cortisone or prednisone. The enzymes responsible for phase I reactions are induced by ethanol and barbiturates and inhibited by chloramphenicol, cimetidine and ethanol.

Phase II reactions involve enzymatic conversion of substances to their acid or salt derivatives, eg, glucuronide, glycine, or sulfate. When the liver is damaged, it is slower in processing of anticonvulsants (phenobarbital), anti-inflammatory agents (acetaminophen or glucocorticoids), tranquilizers (lidocaine, propranolol) or antibiotics (chloramphenicol, tetracycline, or rifampin). In addition, the liver inactivates endogenous hormones by deamination, proteolysis, or deiodination. Glucocorticoids and aldosterone are reduced to their tetrahydro derivative and conjugated to glucuronic acid. Testosterone and estrogen are converted to ketosteroids and conjugated with sulfates or glucuronic acid.

Abnormal physiologic or pathologic conditions of the liver include fatty liver, which is the excessive accumulation of lipids in hepatocytes in response to injury; jaundice, in which large quantities of bilirubin are present in the extracellular fluid; hepatitis, which are viral infections caused by hepadnaviruses but whose major pathology results from host immunologic response; cirrhosis, which is caused by irreversible chronic injury of hepatic parenchyma and progresses to fibrosis; infiltrative diseases such as granulomas and amyloidosis; and adenomas and carcinomas.

Clinicians currently evaluate bilirubin and urobilinogen levels to diagnose hemolytic liver disease and assay carcinoembryonic antigen level to diagnose metastatic cancer. Depending

on its function, an assay for thrombin receptor homolog could become a diagnostic tool for excessive fibrosis and resulting liver damage. If the thrombin receptor homolog is expressed in response to mechanical or chemical injury or involved in unnecessary clotting reactions or progressive fibrosis, then it may also represent an accessible therapeutic target for controlling inflammatory processes in the liver.

Liver anatomy, physiology, and diseases are reviewed, inter alia, in Guyton, AC (1991) Textbook of Medical Physiology, WB Saunders Co, Philadelphia PA; Isselbacher, KJ et al (1994) Harrison's Principles of Internal Medicine, McGraw-Hill, New York City; and The Merck Manual of Diagnosis and Therapy (1992) Merck Research Laboratories, Rahway NJ.

The identification of novel thrombin receptor homologs disclosed in this application provides the opportunity to diagnose or intervene in those signal transduction events associated with inflammation or disease in which such seven transmembrane receptors are expressed or otherwise actively involved.

DISCLOSURE OF THE INVENTION

The subject invention provides a unique nucleotide sequence which encodes a novel human thrombin receptor homolog (TRH). The cDNA, herein designated trh, was identified and cloned using Incyte Clone No. 86700 from a liver cDNA library.

The invention also relates to the use of the nucleotide and amino acid sequences of TRH, or its variants, in the diagnosis and treatment of activated or inflamed cells and/or tissues associated with its expression. Aspects of the invention include the antisense DNA of trh; cloning or expression vectors containing trh; host cells or organisms transformed with expression vectors containing trh; a method for the production and recovery of purified TRH from host cells; and purified protein, TRH, which can be used to identify antagonists, antibodies or inhibitors of the receptor for therapeutic use.

DESCRIPTION OF THE FIGURES

Figures 1A and 1B show the nucleotide (SEQ ID NO:1) and amino acid (SEQ ID NO:2) alignments of the consensus sequence for TRH. The oligomers used to extend the nucleotide sequence to full length are XLR = TGCCTTCCGTTGCTGTATAGACCG and XLF = AAGGAGGGCATAATTCCACAATGTG.

Figure 2 displays the alignment of human TRH with human thrombin receptor, HUMTHRR; boxed residues are identical.

MODES FOR CARRYING OUT THE INVENTION

As used herein, upper case TRH, refers to a thrombin receptor homolog, in either naturally occurring or synthetic form and active fragments thereof, which have the amino acid sequence shown in SEQ ID NO:2. In one embodiment, the polypeptide TRH is encoded by mRNAs transcribed from the cDNA (lower case trh) of SEQ ID NO:1.

5 The novel thrombin receptor homolog (trh) which is the subject of this patent application was identified among the partial cDNAs derived from a liver library. Incyte Clone 86700 is most similar to HUMTHRR, the human thrombin receptor (Dennington PM and MC Berndt (1994) Clin Exp Pharmacol Physiol 21:349-58). Additionally, Incyte 86700 displays amino acid sequence similarity to platelet activating factor receptor, residues 94-10 155. These residues cover most of TMS III, the second intracellular loop, and TMS IV of described seven transmembrane receptors.

"Active" refers to those forms of TRH which retain the biologic and/or immunologic activities of any naturally occurring TRH.

15 "Naturally occurring TRH" refers to TRHs produced by human cells that have not been genetically engineered and specifically contemplates various TRHs arising from post-translational modifications of the polypeptide including but not limited to acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

20 "Derivative" refers to TRHs chemically modified by such techniques as ubiquitination, labeling (eg, with radionuclides, various enzymes, etc), pegylation (derivatization with polyethylene glycol), and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

25 "Recombinant polypeptide variant" refers to any polypeptide having the activity of the TRH polypeptide and differing from naturally occurring TRHs by amino acid insertions, deletions, and substitutions created using recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, such as normal signal transduction, may be found by comparing the sequence of the particular TRH with that of homologous peptides and minimizing the number of amino acid sequence changes made in highly conserved regions.

30 Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, such as the replacement of a leucine with an isoleucine or valine, an aspartate with a glutamate, or a threonine with a serine, ie, conservative replacements. "Insertions" or "deletions" are typically in the range of about 1 to 5 amino acids. The variation allowed may be experimentally determined by producing the peptide synthetically or by systematically making insertions, 35 deletions, or substitutions of nucleotides in a trh molecule using recombinant DNA techniques

and assaying the expressed, recombinant variants for activity.

A polypeptide "fragment", "portion", or "segment" is a stretch of amino acid residues of at least 5 amino acids and as many as about 20 amino acids, preferably about 9 to 13 amino acids. To be active, any TRH fragment must have sufficient length to display biologic and/or immunologic activity either alone or as part of a chimeric display molecule such as keyhole limpet hemocyanin for antibody production or a chimeric test molecule consisting mostly of a purinergic receptor for evaluating activity.

Where desired, a "signal or leader sequence" can direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous sources by recombinant DNA techniques.

"Probe" is an RNA or DNA of sufficient length of use in molecular amplification or hybridization to detect complementary sequences.

An "oligonucleotide" or "oligomer" is a stretch of nucleotide residues which has a sufficient number of bases to be used as a primer or probe in a polymerase chain reaction (PCR). Such oligonucleotides are prepared based on the cDNA sequence which is found in the Sequence Listing. After appropriate testing to establish reaction conditions and to eliminate false positives, they are used to amplify, reveal or confirm the presence of an identical or homologous DNA or its transcribed RNA in a particular cell or tissue. Oligonucleotides or oligomers comprise portions of a DNA sequence having at least about 10 nucleotides and as many as about 35 nucleotides, preferably about 25 nucleotides.

"Degenerate oligonucleotide probes" are probes in which minor substitutions based on the degeneracy of the genetic code (more than one codon may specify the same amino acid) have been made. They are particularly useful in the amplification of a similar natural nucleic acid sequence from chromosomal DNA as described by Walsh PS et al (1992, PCR Methods Appl 1:241-50).

A "portion" or "fragment" of a polynucleotide or nucleic acid comprises all or any part of the nucleotide sequence having fewer nucleotides than about 6 kb, preferably fewer than about 1 kb which can be labelled and used as probe. A probe may be labelled with a radioactive element, an enzyme, or a chromogenic or fluorogenic marker. After appropriate testing to establish reaction conditions and to eliminate false positives, nucleic acid probes may be used in Southern, northern or in situ hybridizations to determine whether DNA or RNA encoding a particular T7G or T7G homolog are present in a particular cell type, tissue, or organ.

Although the sequences for nucleic acid probes may be derived from naturally occurring, recombinant or computer consensus sequences, the physical probe may be chemically synthesized, entirely or in part, and labeled by nick translation, Klenow fill-in reaction, PCR

or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook J et al (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor NY; or Ausubel FM et al (1989) Current Protocols in Molecular Biology, John Wiley & Sons, New York City, both incorporated herein by reference.

"Recombinant nucleotide variants" encoding T7Gs may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce specific restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or to increase expression in a particular prokaryotic or eukaryotic system. Codon usage-specific mutations may also be introduced or chimeras containing the domains of related peptides added to test or modify the properties of any part of the polypeptide, particularly to change ligand-binding affinities, interchain affinities, or degradation/turnover rate.

The present invention provides a unique nucleotide sequence identifying a novel homolog of human thrombin receptor which was first identified among the cDNAs of a liver library. The sequence for trh is shown in SEQ ID NO:1 and is homologous to but significantly different from the GenBank sequence, HUMTHRR. Because TRH may be expressed in cells responding to trauma or infection, the nucleic acid (trh), polypeptide (TRH) and antibodies to TRH are useful in investigations of and interventions in the normal and abnormal physiologic and pathologic processes which regulate cell signalling, immunity, repair, etc. Therefore, an assay for upregulated expression of TRH can accelerate diagnosis and proper treatment of conditions caused by abnormal signal transduction due to systemic and local infections, traumatic and other tissue damage, hereditary or environmental diseases associated with hypertension, carcinomas, and other pathologic problems.

The nucleotide sequence encoding TRH (or its complement) has numerous other applications in techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes for Southern or northern blots, use as oligomers for PCR, use for chromosomal and gene mapping, use in the recombinant production of TRH, use in generation of antisense DNA or RNA, their chemical analogs and the like, and use in production of chimeric molecules for selecting agonists, inhibitors or antagonists for design of domain-specific therapeutic molecules. Uses of the nucleotides encoding TRH disclosed herein are exemplary of known techniques and are not intended to limit their use in any technique known to a person of ordinary skill in the art. Furthermore, the nucleotide sequences disclosed herein may be used in molecular biology techniques that have not yet been developed, provided the new techniques rely on properties of nucleotide sequences that are currently known, eg, the triplet

genetic code, specific base pair interactions, etc.

It will be appreciated by those skilled in the art that as a result of the degeneracy of the genetic code, a multitude of TRH-encoding nucleotide sequences, some bearing minimal homology to the nucleotide sequence of any known and naturally occurring gene may be produced. The invention has specifically contemplated each and every possible variation of nucleotide sequence that could be made by selecting combinations based on possible codon choices. These combinations are made in accordance with the standard triplet genetic code as applied to the nucleotide sequence of naturally occurring TRH, and all such variations are to be considered as being specifically disclosed.

Although nucleotide sequences which encode TRH and its variants are preferably capable of hybridizing to the nucleotide sequence of the naturally occurring TRH gene under stringent conditions, it may be advantageous to produce nucleotide sequences encoding TRH or its derivatives possessing a substantially different codon usage. Codons can be selected to increase the rate at which expression of the peptide occurs in a particular prokaryotic or eukaryotic host in accordance with the frequency with which particular codons are utilized by the host. Other reasons for substantially altering the nucleotide sequence encoding TRH and its derivatives without altering the encoded amino acid sequence include the production of RNA transcripts having more desirable properties, such as a greater half-life, than transcripts produced from the naturally occurring sequence.

The nucleotide sequence encoding TRH may be joined to a variety of other nucleotide sequences by means of well established recombinant DNA techniques (Sambrook J et al, supra). Useful nucleotide sequences for joining to trh include an assortment of cloning vectors such as plasmids, cosmids, lambda phage derivatives, phagemids, and the like that are well known in the art and may be chosen for such characteristics as the size insert they can accommodate, their utility, their fidelity, etc. Other vectors of interest include expression vectors, replication vectors, probe generation vectors, sequencing vectors, YAC and BAC mapping vectors, and the like. In general, these vectors may contain an origin of replication functional in at least one organism, convenient restriction endonuclease sensitive sites, and selectable markers for the host cell.

Another aspect of the subject invention is to provide for trh-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences encoding TRH. Such probes may also be used for the detection of TRH-encoding sequences and should preferably contain at least 50% of the nucleotides from any particular domain of interest from this trh encoding sequence. The hybridization probes of the subject invention may be derived from the nucleotide sequence of the SEQ ID NO:1 or from genomic sequence

including promoter, enhancer elements and introns of the respective naturally occurring trh. Hybridization probes may be labeled by a variety of reporter groups, including radionuclides such as ^{32}P or ^{35}S , or enzymatic labels such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems, and the like.

5 PCR, as described in US Patent Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences which encode TRH. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or may be a mixture of both and comprise a discrete nucleotide sequence for diagnostic use or a degenerate pool of possible sequences for identification of closely related T7G sequences.

10 Full length genes may be cloned from known sequence using a new method as disclosed in Patent Application Serial No 08/487,112, filed June 7, 1995 and hereby incorporated by reference. which employs XL-PCR (Perkin-Elmer, Foster City, CA) to amplify long pieces of DNA. This method was developed to allow a single researcher to process multiple genes (up to 20 or more) at a time and to obtain an extended (possibly full-length) sequence within 6-10
15 days. It replaces current methods which use labelled probes to screen libraries and allow one researcher to process only about 3-5 genes in 14-40 days.

In the first step, which can be performed in about two days, primers are designed and synthesized based on a known partial sequence. In step 2, which takes about six to eight hours, the sequence is extended by PCR amplification of a selected library. Steps 3 and 4, which take
20 about one day, are purification of the amplified cDNA and its ligation into an appropriate vector. Step 5, which takes about one day, involves transforming and growing up host bacteria. In step 6, which takes approximately five hours, PCR is used to screen bacterial clones for extended sequence.

The final steps, which take about one day, involve the preparation and sequencing of
25 selected clones. If the full length cDNA has not been obtained, the entire procedure is repeated using either the original library or some other preferred library. The preferred library may be one that has been size-selected to include only larger cDNAs or may consist of single or combined commercially available libraries, such as lung, liver, heart and brain from Gibco/BRL (Gaithersburg MD). The cDNA library may have been prepared with oligo d(T) or
30 random primers. The advantage of using random primed libraries is that they will have more sequences which contain 5' ends of genes. A randomly primed library may be particularly useful if an oligo d(T) library does not yield a complete gene. Obviously, the larger the protein, the less likely it is that the complete gene will be found in a single plasmid.

Other means for producing hybridization probes for T7G DNAs include the cloning of
35 nucleic acid sequences encoding TRH or its derivatives into vectors for the production of mRNA

probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes in vitro by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA polymerase and the appropriate labeled nucleotides.

It is now possible to produce a DNA sequence, or portions thereof, encoding TRH and/or its derivatives entirely by synthetic chemistry. Such molecules can be inserted into any of the many available vectors using reagents and methods that are known in the art at the time of the filing of this application. Moreover, synthetic chemistry may be used to introduce mutations into the trh sequences or any portion thereof.

The nucleotide sequence can be used to develop an assay to detect activation, inflammation, or disease associated with abnormal levels of TRH expression. The nucleotide sequence can be labeled by methods known in the art and added to a fluid or tissue sample from a patient. After an incubation period sufficient to effect hybridization, the sample is washed with a compatible fluid which contains a visible marker, a dye or other appropriate molecule(s), if the nucleotide has been labeled with an enzyme. After the compatible fluid is rinsed off, the dye is quantitated and compared with a standard. If the amount of dye is significantly elevated (or lowered, as the case may be), the nucleotide sequence has hybridized with the sample, and the assay indicates an abnormal condition such as inflammation or disease.

The nucleotide sequence for trh can be used to construct hybridization probes for mapping the gene. The nucleotide sequence provided herein may be mapped to a chromosome and specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York City.

Fluorescent in situ hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of trh on a physical chromosomal map and a specific disease (or predisposition to a specific disease) can help delimit the region of DNA associated with that genetic disease. The nucleotide sequence of the subject invention may be used to detect differences in gene sequence between normal and carrier or affected individuals.

The nucleotide sequence encoding TRH may be used to produce purified TRH using well known methods of recombinant DNA technology. Among the many publications that teach methods for the expression of genes after they have been isolated is Goeddel (1990) Gene

Expression Technology, Methods and Enzymology, Vol 185, Academic Press, San Diego CA. TRH may be expressed in a variety of host cells, either prokaryotic or eukaryotic. Host cells may be from the same species in which trh nucleotide sequences are endogenous or from a different species. Advantages of producing TRH by recombinant DNA technology include obtaining adequate amounts of the protein for purification and the availability of simplified purification procedures.

Cells transformed with DNA encoding TRH may be cultured under conditions suitable for the expression of TRH and recovery of the protein from the cell culture. TRH produced by a recombinant cell may be secreted or may be contained intracellularly depending on the particular genetic construction used. In general, it is more convenient to prepare recombinant proteins in secreted form. Purification steps vary with the production process and the particular protein produced.

Various methods for the isolation of TRH polypeptide may be accomplished by procedures well known in the art. For example, such a polypeptide may be purified by immunoaffinity chromatography by employing the antibodies provided by the present invention. Various other methods of protein purification well known in the art include those described in Deutscher M (1990) Methods in Enzymology, Vol 182, Academic Press, San Diego CA; and in Scopes R (1982) Protein Purification: Principles and Practice, Springer-Verlag, New York City, both incorporated herein by reference.

In addition to recombinant production, fragments of TRH may be produced by direct peptide synthesis using solid-phase techniques (Stewart et al (1969) Solid-Phase Peptide Synthesis, WH Freeman Co, San Francisco CA; Merrifield J (1963) J Am Chem Soc 85:2149-2154). In vitro protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be achieved, for example, using Applied Biosystems 431A Peptide Synthesizer (ABI, Foster City, California) in accordance with the instructions provided by the manufacturer. Various fragments of TRH may be chemically synthesized separately and combined using chemical methods to produce the full length polypeptide.

TRH for antibody induction does not require biological activity; however, the protein must be antigenic. Peptides used to induce specific antibodies may have an amino acid sequence consisting of at least five amino acids, preferably at least 10 amino acids. They should mimic an exposed structural portion or epitope of the amino acid sequence of the polypeptide and may contain the entire amino acid sequence of a small domain of TRH. Short stretches of TRH amino acids may be fused with those of another protein such as keyhole limpet hemocyanin, and antibody produced against the fusion protein.

Antibodies specific for TRH may be produced by inoculation of an appropriate animal

with the polypeptide or an antigenic fragment. An antibody is specific for TRH if it is specific for an antigenic epitope of the polypeptide and binds to at least part of the natural or recombinant protein. Antibody production includes not only the stimulation of an immune response by injection into animals, but also analogous steps in the production of synthetic antibodies or other specific-binding molecules such as the screening of recombinant immunoglobulin libraries (Orlandi R et al (1989) PNAS 86:3833-37, or Huse WD et al (1989) Science 256:1275-81) or the in vitro stimulation of lymphocyte populations. Current technology (Winter G and Milstein C (1991) Nature 349:293-99) provides for a number of highly specific binding reagents based on the principles of antibody formation. These techniques may be adapted to produce molecules specifically binding particular domains of TRH.

An additional embodiment of the subject invention is the use of TRH specific antibodies or the like as bioactive agents to treat abnormal signal transduction due to systemic and local infections, traumatic and other tissue damage, hereditary or environmental diseases associated with hypertension, carcinomas, and other pathologic problems.

Bioactive compositions comprising agonists, antagonists, or inhibitors of TRH may be administered in a suitable therapeutic dose determined by any of several methodologies including clinical studies on mammalian species to determine maximum tolerable dose and on normal human subjects to determine safe dosage. Additionally, the bioactive agent may be complexed with a variety of well established compounds or compositions which enhance stability or pharmacological properties such as half-life. It is contemplated that a therapeutic, bioactive composition may be delivered by intravenous infusion into the bloodstream or any other effective means which could be used for treatment.

The examples below are provided to describe the subject invention. These examples are provided by way of illustration and are not included for the purpose of limiting the invention.

INDUSTRIAL APPLICABILITY

I Isolation of mRNA and Construction of the cDNA Library

The TRH sequence of this application was first identified in Incyte clone No. 86700 among the sequences comprising the human liver library. The human cells used for this library came from a 49 year old human male (Catalogue # 937224; Stratagene, LaJolla CA). cDNA synthesis for the cDNA library was primed with oligo d(T), and synthetic adaptor oligonucleotides were ligated onto cDNA ends enabling its insertion into Uni-ZAP™ vector system (Stratagene). This allowed high efficiency unidirectional (sense orientation) lambda library construction and the convenience of a plasmid system with blue/white color selection to

detect clones with cDNA insertions.

The cDNA library can be screened with either DNA probes or antibody probes and the pBluescript® phagemid (Stratagene) can be rapidly excised in vivo. The phagemid allows the use of a plasmid system for easy insert characterization, sequencing, site-directed
5 mutagenesis, the creation of unidirectional deletions and expression of fusion polypeptides. The custom-constructed library phage particles were infected into E. coli host strain XL1-Blue® (Stratagene), which has a high transformation efficiency, increasing the probability of obtaining rare, under-represented clones in the cDNA library. Alternative unidirectional vectors include but are not limited to pcDNA1 (Invitrogen, San Diego CA) and pSHlox-1
10 (Novagen, Madison WI).

I I Isolation of cDNA Clones

The phagemid forms of individual cDNA clones were obtained by the in vivo excision process, in which the host bacterial strain was coinfectd with both the library phage and an f1
15 helper phage. Polypeptides or enzymes derived from both the library-containing phage and the helper phage nicked the DNA, initiated new DNA synthesis from defined sequences on the target DNA and created a smaller, single stranded circular phagemid DNA molecule that included all DNA sequences of the pBLUESCRIPT® plasmid and the cDNA insert. The phagemid DNA was secreted from the cells and purified, then used to re-infect fresh host cells, where double
20 stranded phagemid DNA was produced. Because the phagemid carries the gene for β -lactamase, the newly transformed bacteria were selected on medium containing ampicillin.

Phagemid DNA was purified using the MAGIC MINIPREPS™ DNA Purification System (Catalogue #A7100; Promega Corp, Madison, WI). This small-scale process provides a simple and reliable method for lysing the bacterial cells and rapidly isolating purified phagemid
25 DNA using a proprietary DNA-binding resin. Phagemid DNA was also purified using the QIAWELL-8 Plasmid Purification System (QIAGEN Inc, Chatsworth CA). This product line provides a convenient, rapid high-throughput method for lysing the bacterial cells and isolating highly purified phagemid DNA using QIAGEN anion-exchange resin particles. Following either purification method, the DNA was eluted and prepared for sequencing and other analytical
30 manipulations.

I I I Sequencing of cDNA Clones

The cDNA inserts from random isolates of the liver library were sequenced in part. Methods for DNA sequencing are well known in the art. Conventional enzymatic methods
35 employed DNA polymerase Klenow fragment, SEQUENASE® (US Biochemical Corp, Cleveland OH)

or Taq polymerase to extend DNA chains from an oligonucleotide primer annealed to the DNA template of interest. Methods have been developed for the use of both single- and double-stranded templates. The chain termination reaction products were electrophoresed on urea-acrylamide gels and detected either by autoradiography (for radionuclide-labeled precursors) or by fluorescence (for fluorescent-labeled precursors). Recent improvements in mechanized reaction preparation, sequencing and analysis using the fluorescent detection method have permitted expansion in the number of sequences that can be determined per day using machines such as the Catalyst 800 and the Applied Biosystems 377 or 373 DNA sequencers.

IV Homology Searching of cDNA Clones and Deduced Proteins

Each sequence so obtained was compared to sequences in GenBank using a search algorithm developed by Applied Biosystems and incorporated into the INHERIT™ 670 Sequence Analysis System. In this algorithm, Pattern Specification Language (developed by TRW Inc., Los Angeles CA) was used to determine regions of homology. The three parameters that determine how the sequence comparisons run were window size, window offset, and error tolerance. Using a combination of these three parameters, the DNA database was searched for sequences containing regions of homology to the query sequence, and the appropriate sequences were scored with an initial value. Subsequently, these homologous regions were examined using dot matrix homology plots to distinguish regions of homology from chance matches. Smith-Waterman alignments were used to display the results of the homology search.

Peptide and protein sequence homologies were ascertained using the INHERIT™ 670 Sequence Analysis System in a way similar to that used in DNA sequence homologies. Pattern Specification Language and parameter windows were used to search protein databases for sequences containing regions of homology which were scored with an initial value. Dot-matrix homology plots were examined to distinguish regions of significant homology from chance matches.

Alternatively, BLAST, which stands for Basic Local Alignment Search Tool, is used to search for local sequence alignments (Altschul SF (1993) J Mol Evol 36:290-300; Altschul, SF et al (1990) J Mol Biol 215:403-10). BLAST produces alignments of both nucleotide and amino acid sequences to determine sequence similarity. Because of the local nature of the alignments, BLAST is especially useful in determining exact matches or in identifying homologs. Whereas it is ideal for matches which do not contain gaps, it is inappropriate for performing motif-style searching. The fundamental unit of BLAST algorithm output is the High-scoring Segment Pair (HSP).

An HSP consists of two sequence fragments of arbitrary but equal lengths whose alignment is locally maximal and for which the alignment score meets or exceeds a threshold or cutoff score set by the user. The BLAST approach is to look for HSPs between a query sequence and a database sequence, to evaluate the statistical significance of any matches found, and to report only those matches which satisfy the user-selected threshold of significance. The parameter E establishes the statistically significant threshold for reporting database sequence matches. E is interpreted as the upper bound of the expected frequency of chance occurrence of an HSP (or set of HSPs) within the context of the entire database search. Any database sequence whose match satisfies E is reported in the program output.

V Identification, Full Length Cloning, Sequencing and Translation

Analysis of INHERIT™ results from randomly picked and sequenced portions of clones from liver library identified Incyte 86700 as a homolog of the thrombin receptor, HUMTHRR. The cDNA insert comprising Incyte 86700 was fully sequenced and used as the basis for cloning the full length cDNA.

The cDNA of Incyte Clone 86700 was extended to full length using a modified XL-PCR (Perkin Elmer) procedure as disclosed in Patent Application Serial No 08/487,112, by Guegler et al, filed June 7, 1995 and hereby incorporated by reference. Primers were designed based on known sequence; one primer was synthesized to initiate extension in the antisense direction (XLR = TGCCTTCCGTTGCTGTATAGACCG) and the other to extend sequence in the sense direction (XLF = AAGGAGGGCATAATTCCACAATGTG). The primers allowed the sequence to be extended "outward" generating amplicons containing new, unknown nucleotide sequence for the gene of interest. The primers were designed using Oligo 4.0 (National Biosciences Inc, Plymouth MN) to be 22-30 nucleotides in length, to have a GC content of 50% or more, and to anneal to the target sequence at temperatures about 68°-72° C. Any stretch of nucleotides which would result in hairpin structures and primer-primer dimerizations were avoided.

The liver cDNA library was used as a template, and XLR and XLF primers were used to extend and amplify the 86700 sequence. By following the instructions for the XL-PCR kit and thoroughly mixing the enzyme and reaction mix, high fidelity amplification is obtained. Beginning with 25 pMol of each primer and the recommended concentrations of all other components of the kit, PCR was performed using the MJ thermocycler PTC200 (MJ Research, Watertown MA) and the following parameters:

Step 1	94° C for 60 sec (initial denaturation)
Step 2	94° C for 15 sec

- Step 3 65° C for 1 min
- Step 4 68° C for 7 min
- Step 5 Repeat step 2-4 for 15 additional times
- Step 6 94° C for 15 sec
- 5 Step 7 65° C for 1 min
- Step 8 68° C for 7 min + 15 sec/cycle
- Step 9 Repeat step 6-8 for 11 additional times
- Step 10 72° C for 8 min
- Step 11 4° C (and holding)

10 At the end of 28 cycles, 50 µl of the reaction mix was removed; and the remaining reaction mix was run for an additional 10 cycles as outlined below:

- Step 1 94° C for 15 sec
- Step 2 65° C for 1 min
- Step 3 68° C for (10 min + 15 sec)/cycle
- 15 Step 4 Repeat step 1-3 for 9 additional times
- Step 5 72° C for 10 min

20 A 5-10 µl aliquot of the reaction mixture was analyzed by electrophoresis on a low concentration (about 0.6-0.8%) agarose mini-gel to determine which reactions were successful in extending the sequence. Although all extensions potentially contain a full length gene, some of the largest products or bands were selected and cut out of the gel. Further purification involved using a commercial gel extraction method such as QIAQuick™ (QIAGEN Inc, Chatsworth CA). After recovery of the DNA, Klenow enzyme was used to trim single-stranded, nucleotide overhangs creating blunt ends which facilitated religation and cloning.

25 After ethanol precipitation, the products were redissolved in 13 µl of ligation buffer. Then, 1µl T4-DNA ligase (15 units) and 1µl T4 polynucleotide kinase were added, and the mixture was incubated at room temperature for 2-3 hours or overnight at 16° C. Competent E. coli cells (in 40 µl of appropriate media) were transformed with 3 µl of ligation mixture and cultured in 80 µl of SOC medium (Sambrook J et al, supra). After incubation for one hour at 37° C, the whole transformation mixture was plated on Luria Bertani (LB)-agar (Sambrook J et al, supra) containing carbenicillin at 25 mg/L. The following day, 12 colonies were

30 randomly picked from each plate and cultured in 150 µl of liquid LB/carbenicillin medium placed in an individual well of an appropriate, commercially-available, sterile 96-well microtiter plate. The following day, 5 µl of each overnight culture was transferred into a non-sterile 96-well plate and after dilution 1:10 with water, 5 µl of each sample was transferred

35 into a PCR array.

For PCR amplification, 15 µl of concentrated PCR reaction mix (1.33X) containing 0.75 units of Taq polymerase, a vector primer and one or both of the gene specific primers used for the extension reaction were added to each well. Amplification was performed using the following conditions:

- Step 1 94° C for 60 sec
- Step 2 94° C for 20 sec
- Step 3 55° C for 30 sec
- Step 4 72° C for 90 sec
- Step 5 Repeat steps 2-4 for an additional 29 times
- Step 6 72° C for 180 sec
- Step 7 4° C (and holding)

Aliquots of the PCR reactions were run on agarose gels together with molecular weight markers. The sizes of the PCR products were compared to the original partial cDNAs, and appropriate clones were selected, ligated into plasmid and sequenced.

The cDNA (SEQ ID NO:1) and amino acid (SEQ ID NO:2) sequences for human TRH are shown in Figure 1. When the three possible translations of TRH were searched against protein databases such as SwissProt and PIR, no exact matches were found. Fig 2 shows the comparison between the trh and HUMTHRR sequences.

VI Antisense analysis

Knowledge of the correct, complete cDNA sequence of TRH enables its use as a tool for antisense technology in the investigation of gene function. Oligonucleotides, cDNA or genomic fragments comprising the antisense strand of trh are used either in vitro or in vivo to inhibit expression of the mRNA. Such technology is now well known in the art, and antisense molecules are designed at various locations along the nucleotide sequences. By treatment of cells or whole test animals with such antisense sequences, the gene of interest can be effectively turned off. Frequently, the function of the gene is ascertained by observing behavior at the intracellular, cellular, tissue or organismal level (eg, lethality, loss of differentiated function, changes in morphology, etc).

In addition to using sequences constructed to interrupt transcription of a particular open reading frame, modifications of gene expression are obtained by designing antisense sequences to intron regions, promoter/enhancer elements, or even to trans-acting regulatory genes. Similarly, inhibition is achieved using Hogeboom base-pairing methodology, also known as "triple helix" base pairing.

VII Expression of TRH

Expression of trh is accomplished by subcloning the cDNAs into appropriate expression vectors and transfecting the vectors into analogous expression hosts. In this particular case, the cloning vector previously used for the generation of the cDNA library, pBluescript, also provides for direct expression of trh sequences in E. coli. Upstream of the cloning site, this vector contains a promoter for β -galactosidase, followed by sequence containing the amino-terminal Met and the subsequent 7 residues of β -galactosidase. Immediately following these eight residues is an engineered bacteriophage promoter useful for artificial priming and transcription and a number of unique restriction sites, including Eco RI, for cloning.

Induction of the isolated, transfected bacterial strain with IPTG using standard methods produces a fusion protein corresponding to the first seven residues of β -galactosidase, about 15 residues of "linker", and the peptide encoded within the cDNA. Since cDNA clone inserts are generated by an essentially random process, there is one chance in three that the included cDNA lies in the correct frame for proper translation. If the cDNA is not in the proper reading frame, it is obtained by deletion or insertion of the appropriate number of bases by well known methods including in vitro mutagenesis, digestion with exonuclease III or mung bean nuclease, or the inclusion of an oligonucleotide linker of appropriate length.

Alternatively, the trh cDNA is shuttled into other vectors known to be useful for expression of protein in specific hosts. Oligonucleotide primers containing cloning sites as well as a segment of DNA (about 25 bases) sufficient to hybridize to stretches at both ends of the target cDNA is synthesized chemically by standard methods. These primers are then used to amplify the desired gene segment by PCR. The resulting gene segment is digested with appropriate restriction enzymes under standard conditions and isolated by gel electrophoresis. Alternately, similar gene segments are produced by digestion of the cDNA with appropriate restriction enzymes. Using appropriate primers, segments of coding sequence from more than one gene are ligated together and cloned in appropriate vectors. It is possible to optimize expression by construction of such chimeric sequences.

Suitable expression hosts for such chimeric molecules include, but are not limited to, mammalian cells such as Chinese Hamster Ovary (CHO) and human 293 cells, insect cells such as Sf9 cells, yeast cells such as Saccharomyces cerevisiae, and bacteria such as E. coli. For each of these cell systems, a useful expression vector includes an origin of replication to allow propagation in bacteria and a selectable marker such as the β -lactamase antibiotic resistance gene to allow plasmid selection in bacteria. In addition, the vector includes a second selectable marker such as the neomycin phosphotransferase gene to allow selection in transfected eukaryotic host cells. Vectors for use in eukaryotic expression hosts often require RNA

processing elements such as 3' polyadenylation sequences if such are not part of the cDNA of interest.

Additionally, the vector contains promoters or enhancers which increase gene expression. Such promoters are host specific and include MMTV, SV40, and metallothionine promoters for CHO cells; trp, lac, tac and T7 promoters for bacterial hosts; and alpha factor, alcohol oxidase and PGH promoters for yeast. Transcription enhancers, such as the rous sarcoma virus enhancer, are used in mammalian host cells. Once homogeneous cultures of recombinant cells are obtained through standard culture methods, large quantities of recombinantly produced TRH are recovered from the conditioned medium and analyzed using chromatographic methods known in the art.

VIII Isolation of Recombinant TRH

TRH is expressed as a chimeric protein with one or more additional polypeptide domains added to facilitate protein purification. Such purification facilitating domains include, but are not limited to, metal chelating peptides such as histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp, Seattle WA). The inclusion of a cleavable linker sequence such as Factor XA or enterokinase (Invitrogen, San Diego CA) between the purification domain and the trh sequence is useful to facilitate expression of TRH.

IX Testing of Chimeric T7Gs

Functional chimeric T7Gs are constructed by combining the extracellular receptive sequences of a new isoform with the transmembrane and intracellular segments of a known isoform. Such chimeric molecules are useful for testing purposes. This concept was demonstrated by Kobilka et al (1988, Science 240:1310-1316) who created a series of chimeric $\alpha 2$ - $\beta 2$ adrenergic receptors (AR) by inserting progressively greater amounts of $\alpha 2$ -AR transmembrane sequence into $\beta 2$ -AR. The binding activity of known agonists changed as the molecule shifted from having more $\alpha 2$ than $\beta 2$ conformation, and intermediate constructs demonstrated mixed specificity. The specificity for binding antagonists, however, correlated with the source of the domain VII. The importance of T7G domain VII for ligand recognition was also found in chimeras utilizing two yeast α -factor receptors and is significant because the yeast receptors are classified as miscellaneous receptors. Thus, the functional role of specific domains appears to be preserved throughout the T7G family regardless of category.

In parallel fashion, internal segments or cytoplasmic domains from a particular

isoform are exchanged with the analogous domains of a known T7G and used to identify the structural determinants responsible for coupling the receptors to trimeric G-proteins (Dohlman et al (1991) Annu Rev Biochem 60:653-88). A chimeric receptor in which domains V, VI, and the intracellular connecting loop from $\beta 2$ -AR are substituted into $\alpha 2$ -AR are shown to bind ligands with $\alpha 2$ -AR specificity, but to stimulate adenylate cyclase in the manner of $\beta 2$ -AR. This demonstrates that for adrenergic-type receptors, G-protein recognition is present in domains V and VI and their connecting loop. The opposite situation was predicted and observed for a chimera in which the V->VI loop from $\alpha 1$ -AR replaced the corresponding domain on $\beta 2$ -AR and the resulting receptor bound ligands with $\beta 2$ -AR specificity and activated G-protein-mediated phosphatidylinositol turnover in the $\alpha 1$ -AR manner. Finally, chimeras constructed from muscarinic receptors also demonstrated that V->VI loop is the major determinant for specificity of G-protein activity (Bolander, supra).

Chimeric or modified T7Gs containing substitutions in the extracellular and transmembrane regions have shown that both portions of the receptor determine ligand binding specificity. For example, two Ser residues are conserved in domain V of all adrenergic and D catecholamine receptors and are necessary for potent agonist activity. These serines are believed to be in the T7G binding site and to form hydrogen bonds with the catechol moiety of the agonists. Similarly, an Asp residue present in domain III of all T7Gs which binds biogenic amines is believed to be in the T7G binding site and to form an ion pair with the ligand amine group.

Functional, cloned T7Gs are expressed in heterologous expression systems and their biological activity is assessed (Marullo et al (1988) Proc Natl Acad Sci 85:7551-55; King et al (1990) Science 250:121-23). One heterologous system introduces genes for a mammalian T7G and a mammalian G-protein into yeast cells. The T7G was shown to have appropriate ligand specificity and affinity and to trigger appropriate biological activation--growth arrest and morphological changes--of the yeast cells. Novel sequences for T7G domains are tested in a similar manner.

X Production of TRH Specific Antibodies

Two approaches are utilized to raise antibodies to TRH, and each approach is useful for generating either polyclonal or monoclonal antibodies. In one approach, denatured protein from reverse phase HPLC separation is obtained in quantities up to 75 mg. This denatured protein is used to immunize mice or rabbits using standard protocols; about 100 micrograms are adequate for immunization of a mouse, while up to 1 mg might be used to immunize a rabbit. For identifying mouse hybridomas, the denatured protein is radioiodinated and used to screen

potential murine B-cell hybridomas for those which produce antibody. This procedure requires only small quantities of protein, such that 20 mg would be sufficient for labeling and screening of several thousand clones.

In a second approach, the amino acid sequence of an appropriate TRH domain, as deduced from translation of the cDNA, is analyzed to determine regions of high immunogenicity. Oligopeptides comprising appropriate hydrophilic regions, as illustrated in Figure 3, are synthesized and used in suitable immunization protocols to raise antibodies. Analysis to select appropriate epitopes is described by Ausubel FM et al (supra). The optimal amino acid sequences for immunization are usually at the C-terminus, the N-terminus and those intervening, hydrophilic regions of the polypeptide which are likely to be exposed to the external environment when the protein is in its natural conformation.

Typically, selected peptides, about 15 residues in length, are synthesized using an Applied Biosystems Peptide Synthesizer Model 431A using fmoc-chemistry and coupled to keyhole limpet hemocyanin (KLH; Sigma, St Louis MO) by reaction with M-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS; Ausubel FM et al, supra). If necessary, a cysteine is introduced at the N-terminus of the peptide to permit coupling to KLH. Rabbits are immunized with the peptide-KLH complex in complete Freund's adjuvant. The resulting antisera are tested for antipeptide activity by binding the peptide to plastic, blocking with 1% bovine serum albumin, reacting with antisera, washing and reacting with labeled (radioactive or fluorescent), affinity purified, specific goat anti-rabbit IgG.

Hybridomas are prepared and screened using standard techniques. Hybridomas of interest are detected by screening with labeled TRH to identify those fusions producing the monoclonal antibody with the desired specificity. In a typical protocol, wells of plates (FAST; Becton-Dickinson, Palo Alto CA) are coated during incubation with affinity purified, specific rabbit-anti-mouse (or suitable anti-species Ig) antibodies at 10 mg/ml. The coated wells are blocked with 1% BSA, washed and incubated with supernatants from hybridomas. After washing the wells are incubated with labeled TRH at 1 mg/ml. Supernatants with specific antibodies bind more labeled TRH than is detectable in the background. Then clones producing specific antibodies are expanded and subjected to two cycles of cloning at limiting dilution. Cloned hybridomas are injected into pristane-treated mice to produce ascites, and monoclonal antibody is purified from mouse ascitic fluid by affinity chromatography on Protein A. Monoclonal antibodies with affinities of at least 10^8 M^{-1} , preferably 10^9 to 10^{10} or stronger, are typically produced by standard procedures as described in Harlow and Lane (1988) Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY; and in Goding (1986) Monoclonal Antibodies: Principles and Practice, Academic Press, New York NY, both

incorporated herein by reference.

XI Diagnostic Test Using TRH Specific Antibodies

Particular TRH antibodies are useful for investigating signal transduction and the
5 diagnosis of infectious or hereditary conditions which are characterized by differences in the
amount or distribution of TRH or downstream products of an active signaling cascade. Since TRH
was found in a human liver library, it appears to be upregulated in cell types mainly involved
in immune protection or defense.

Diagnostic tests for TRH include methods utilizing antibody and a label to detect TRH in
10 human body fluids, membranes, cells, tissues or extracts of such. The polypeptides and
antibodies of the present invention are used with or without modification. Frequently, the
polypeptides and antibodies are labeled by joining them, either covalently or noncovalently,
with a substance which provides for a detectable signal. A wide variety of labels and conjugation
15 techniques are known and have been reported extensively in both the scientific and patent
literature. Suitable labels include radionuclides, enzymes, substrates, cofactors, inhibitors,
fluorescent agents, chemiluminescent agents, magnetic particles and the like. Patents teaching
the use of such labels include US Patent Nos. 3,817,837; 3,850,752; 3,939,350;
3,996,345; 4,277,437; 4,275,149; and 4,366,241. Also, recombinant immunoglobulins
are produced as shown in US Patent No. 4,816,567, incorporated herein by reference.

20 A variety of protocols for measuring soluble or membrane-bound TRH, using either
polyclonal or monoclonal antibodies specific for the protein, are known in the art. Examples
include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA) and
fluorescent activated cell sorting (FACS). A two-site monoclonal-based immunoassay utilizing
monoclonal antibodies reactive to two non-interfering epitopes on TRH is preferred, but a
25 competitive binding assay may be employed. These assays are described, among other places, in
Maddox, DE et al (1983, J Exp Med 158:1211f).

XII Purification of Native TRH Using Specific Antibodies

Native or recombinant TRH is purified by immunoaffinity chromatography using
30 antibodies specific for TRH. In general, an immunoaffinity column is constructed by covalently
coupling the anti-TRH antibody to an activated chromatographic resin.

Polyclonal immunoglobulins are prepared from immune sera either by precipitation
with ammonium sulfate or by purification on immobilized Protein A (Pharmacia LKB
Biotechnology, Piscataway, NJ). Likewise, monoclonal antibodies are prepared from mouse
35 ascites fluid by ammonium sulfate precipitation or chromatography on immobilized Protein A.

Partially purified immunoglobulin is covalently attached to a chromatographic resin such as CnBr-activated Sepharose (Pharmacia, Piscataway NJ). The antibody is coupled to the resin, the resin is blocked, and the derivative resin is washed according to the manufacturer's instructions.

5 Such immunoaffinity columns are utilized in the purification of TRH by preparing a fraction from cells containing TRH in a soluble form. This preparation is derived by solubilization of whole cells or of a subcellular fraction obtained via differential centrifugation (with or without addition of detergent) or by other methods well known in the art. Alternatively, soluble TRH containing a signal sequence is secreted in useful quantity into the
10 medium in which the cells are grown.

 A soluble TRH-containing preparation is passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of TRH (eg, high ionic strength buffers in the presence of detergent). Then, the column is eluted under conditions that disrupt antibody/TRH binding (eg, a buffer of pH 2-3 or a high concentration of
15 a chaotrope such as urea or thiocyanate ion), and TRH is collected.

XIII Drug Screening

 This invention is particularly useful for screening therapeutic compounds by using TRH or binding fragments thereof in any of a variety of drug screening techniques. The polypeptide
20 or fragment employed in such a test is either free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide, fragment or chimera as described above. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, are
25 used for standard binding assays. The formation of complexes between TRH and the agent being tested are measured. Alternatively, one examines the diminution in complex formation between TRH and a receptor caused by the agent being tested.

 Thus, the present invention provides methods of screening for drugs or any other agents which affect signal transduction. These methods, well known in the art, comprise contacting
30 such an agent with TRH polypeptide or a fragment thereof and assaying (i) for the presence of a complex between the agent and the TRH polypeptide or fragment, or (ii) for the presence of a complex between the TRH polypeptide or fragment and the cell. In such competitive binding assays, the TRH polypeptide or fragment is typically labeled. After suitable incubation, free TRH polypeptide or fragment is separated from that present in bound form, and the amount of
35 free or uncomplexed label is a measure of the ability of the particular agent to bind to TRH or to

interfere with the formation of the TRH and agent complex.

Another technique for drug screening provides high throughput screening for compounds having suitable binding affinity to the TRH polypeptides and is described in detail in European Patent Application 84/03564, published on September 13, 1984, incorporated herein by reference. Briefly stated, large numbers of different small peptide test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. The peptide test compounds are reacted with TRH polypeptide and washed. Bound TRH polypeptide is then detected by methods well known in the art. Alternatively, purified TRH is coated directly onto plates for use in the aforementioned drug screening techniques. In addition, non-neutralizing antibodies are used to capture the peptide and immobilize it on the solid support.

This invention also contemplates the use of competitive drug screening assays in which neutralizing antibodies capable of binding TRH specifically compete with a test compound for binding to TRH polypeptides or fragments thereof. In this manner, the antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with TRH.

XIV Rational Drug Design

The goal of rational drug design is to produce structural analogs of biologically active polypeptides of interest or of small molecules with which they interact, eg, agonists, antagonists, or inhibitors. Any of these examples can be used to fashion drugs which are more active or stable forms of the polypeptide or which enhance or interfere with the function of a polypeptide in vivo (Hodgson J (1991) Bio/Technology 9:19-21, incorporated herein by reference).

In one approach, the three-dimensional structure of a protein of interest, or of a protein-inhibitor complex, is determined by x-ray crystallography, by computer modeling or, most typically, by a combination of the two approaches. Both the shape and charges of the polypeptide must be ascertained to elucidate the structure and to determine active site(s) of the molecule. Less often, useful information regarding the structure of a polypeptide is gained by modeling based on the structure of homologous proteins. In both cases, relevant structural information is used to design efficient inhibitors. Useful examples of rational drug design include molecules which have improved activity or stability as shown by Braxton S and Wells JA (1992, Biochemistry 31:7796- 7801) or which act as inhibitors, agonists, or antagonists of native peptides as shown by Athauda SB et al (1993 J Biochem 113:742-46), incorporated herein by reference.

It is also possible to isolate a target-specific antibody, selected by functional assay, as described above, and then to solve its crystal structure. This approach, in principle, yields a

pharmacore upon which subsequent drug design is based. It is possible to bypass protein crystallography altogether by generating anti-idiotypic antibodies (anti-ids) to a functional, pharmacologically active antibody. As a mirror image of a mirror image, the binding site of the anti-ids is expected to be an analog of the original receptor. The anti-id is then used to identify and isolate peptides from banks of chemically or biologically produced peptides. The isolated peptides then act as the pharmacore.

By virtue of the present invention, sufficient amount of polypeptide are made available to perform such analytical studies as X-ray crystallography. In addition, knowledge of the TRH amino acid sequence provided herein provide guidance to those employing computer modeling techniques in place of or in addition to x-ray crystallography.

XV Identification of Other Members of the Signal Transduction Complex

Purified TRH is a research tool for identification, characterization and purification of interacting G-proteins, phospholipase C, adenylate cyclase, or other signal transduction pathway proteins. Radioactive labels are incorporated into a selected TRH domain by various methods known in the art and used *in vitro* to capture interacting molecules. A preferred method involves labeling the primary amino groups in TRH with ¹²⁵I Bolton-Hunter reagent (Bolton, AE and Hunter, WM (1973) Biochem J 133: 529). This reagent has been used to label various molecules without concomitant loss of biological activity (Hebert CA et al (1991) J Biol Chem 266: 18989; McColl S et al (1993) J Immunol 150:4550-4555).

Labeled TRH is useful as a reagent for the purification of molecules with which it interacts. In one embodiment of affinity purification, membrane-bound TRH is covalently coupled to a chromatography column. Cell-free extract derived from library or target cells is passed over the column, and molecules with appropriate affinity bind to TRH. The TRH-complex is recovered from the column, dissociated and the recovered molecule is subjected to N-terminal protein sequencing. This amino acid sequence is then used to identify the captured molecule or to design degenerate oligonucleotide probes for cloning the relevant gene from an appropriate DNA library.

In an alternate method, antibodies are raised against TRH, specifically monoclonal antibodies, as described above. The monoclonal antibodies are screened to identify those which inhibit the binding between ligands and TRH. These monoclonal antibodies are then used therapeutically.

XVI Use and Administration of Antibodies, Inhibitors, or Antagonists

Antibodies, inhibitors, or antagonists of TRH (or other treatments to limit signal

transduction, LST), provide different effects when administered therapeutically. LSTs are formulated in a nontoxic, inert, pharmaceutically acceptable aqueous carrier medium preferably at a pH of about 5 to 8, more preferably 6 to 8, although pH varies according to the characteristics of the antibody, inhibitor, or antagonist being formulated and the condition to be treated. Characteristics of LSTs include solubility of the molecule, half-life and antigenicity/immunogenicity; these and other characteristics aid in defining an effective carrier. Native human proteins are preferred as LSTs, but organic or synthetic molecules resulting from drug screens are equally effective in particular situations.

LSTs are delivered by known routes of administration including but not limited to topical creams and gels; transmucosal spray and aerosol; transdermal patch and bandage; injectable, intravenous and lavage formulations; and orally administered liquids and pills particularly formulated to resist stomach acid and enzymes. The particular formulation, exact dosage, and route of administration is determined by the attending physician and varies according to each specific situation.

Such determinations are made by considering multiple variables such as the condition to be treated, the LST to be administered, and the pharmacokinetic profile of the particular LST. Additional factors which are taken into account include disease state (eg, severity) of the patient, age, weight, gender, diet, time and frequency of administration, drug combination, reaction sensitivities, and tolerance/response to therapy. Long acting LST formulations are administered every 3 to 4 days, every week, or once every two weeks depending on half-life and clearance rate of the particular LST.

Normal dosage amounts vary from 0.1 to 100,000 micrograms, up to a total dose of about 1 g, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature. See US Patent Nos. 4,657,760; 5,206,344; or 5,225,212. Those skilled in the art employ different formulations for different LSTs. Administration to cells such as nerve cells necessitates delivery in a manner different from that to other cells such as vascular endothelial cells.

It is contemplated that abnormal signal transduction in those conditions or diseases which trigger mast cell activity cause damage that is treatable with LSTs. Such conditions, particularly anaphylactic or hypersensitive responses, are treated as discussed above. The LST is also used to treat other systemic and local infections, traumatic tissue damage, hereditary or environmental diseases associated with allergies, hypertension, carcinoma, and other physiologic/pathologic problems associated with abnormal signal transduction.

All publications and patents mentioned in the above specification are herein incorporated

by reference. Various modifications and variations of the described method and system of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with specific preferred embodiments, it should be understood that the invention as claimed should not be
5 unduly limited to such specific embodiments. Indeed, various modifications of the above-described modes for carrying out the invention which are obvious to those skilled in the field of molecular biology or related fields are intended to be within the scope of the following claims.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: INCYTE PHARMACEUTICALS, INC.
- (ii) TITLE OF INVENTION: THROMBIN RECEPTOR HOMOLOG
- (iii) NUMBER OF SEQUENCES: 3
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 - (B) STREET: 3330 Hillview Avenue
 - (C) CITY: Palo Alto
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: To Be Assigned
 - (B) FILING DATE: Filed Herewith
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/467,125
 - (B) FILING DATE: 6-JUN-1995
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Luther, Barbara J.
 - (B) REGISTRATION NUMBER: 33954
 - (C) REFERENCE/DOCKET NUMBER: PF-0041 PCT
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 415-855-0555
 - (B) TELEFAX: 415-852-0195

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1143 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: Liver
 - (B) CLONE: 86700
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGAGAAGTC ATACCATAAC AATGACGACA ACTTCAGTCA GCAGCTGGCC TTACTCCTCC 60
 CACAGAATGC GCTTTATAAC CAATCATAGC GACCAACCGC CACAAAACCTT CTCAGCAACA 120
 CCAAATGTTA CTACCTGTCC CATGGATGAA AAATTGCTAT CTACTGTGTT AACCACATCC 180
 TACTCTGTTA TTTTCATCGT GGGACTGGTT GGAACATAA TCGCCCCCTA TGTATTTCTG 240
 GGTATTCACC GTAAAAGAAA TTCCATTCAA ATTTATCTAC TTAACGTAGC CATTGCAGAC 300
 CTCCTACTCA TCTTCTGCCT CCCTTTCCGA ATAATGTATC ATATTAACCA AAACAAGTGG 360
 AACTAGGTG TGATTCTGTG CAAGGTTGTG GGAACACTGC TTTATATGAA CATGTACATT 420
 AGCATTATTT TGCTTGGATT CATCAGTTTG GATCGCTATA TAAAAATTAA TCGGTCTATA 480
 CAGCAACGGA AGGCAATAAC AACCAACAA AGTATTTATG TCTGTTGTAT AGTATGGATG 540
 CTTGCTCTTG GTGGATTCTT AACTATGATT ATTTTAACAC TTAAGAAAGG AGGGCATAAT 600
 TCCACAATGT GTTTCCATTA CAGAGATAAG CATAACGCAA AAGGAGAAGC CATTTTTAAC 660
 TTCATTCTTG TGGTAATGTT CTGGCTAATT TTCTTACTAA TAATCCTTTC ATATATTAAG 720
 ATTGGGAAGA ATCTATTGAG GATTTCTAAA AGGAGGTCAA AATTTCTTAA TTCTGGTAAA 780
 TATGCCACTA CAGCTCGTAA CTCCTTTATT GTACTTATCA TTTTACTAT ATGTGTGGGT 840
 CCCTATCATG CCTTTGATT CATCTACATT TCTTCACAGC TAAATGTATC ATCTTGCTAC 900
 TGGAAAGAAA TTGTTCAAA AACCAATGAG ATCATGCTGG TTCTCTCATC TTTCAATAGT 960
 TGGTTAGATC CAGTCATGTA TTTCTGATG TCCAGTAACA TTCGAAAAT AATGTGCCAA 1020
 CTTCTTTTGA GACGATTTC AAGTGAACCA AGTAGGAGTG AAAGCACTTC AGAATTTAAA 1080
 CCAGGATACT CCCTGCATGA TACATCTGTG GCAGGGAAAA TACAGTCTAG TTCTGAAAGT 1140
 ACT 1143

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Liver
- (B) CLONE: 86700

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Arg Ser His Thr Ile Thr Met Thr Thr Thr Ser Val Ser Ser Trp
 1 5 10 15
 Pro Tyr Ser Ser His Arg Met Arg Phe Ile Thr Asn His Ser Asp Gln
 20 25 30
 Pro Pro Gln Asn Phe Ser Ala Thr Pro Asn Val Thr Thr Cys Pro Met
 35 40 45
 Asp Glu Lys Leu Leu Ser Thr Val Leu Thr Thr Ser Tyr Ser Val Ile
 50 55 60
 Phe Ile Val Gly Leu Val Gly Asn Ile Ile Ala Pro Tyr Val Phe Leu
 65 70 75 80
 Gly Ile His Arg Lys Arg Asn Ser Ile Gln Ile Tyr Leu Leu Asn Val
 85 90 95
 Ala Ile Ala Asp Leu Leu Leu Ile Phe Cys Leu Pro Phe Arg Ile Met
 100 105 110
 Tyr His Ile Asn Gln Asn Lys Trp Thr Leu Gly Val Ile Leu Cys Lys
 115 120 125
 Val Val Gly Thr Leu Leu Tyr Met Asn Met Tyr Ile Ser Ile Ile Leu
 130 135 140
 Leu Gly Phe Ile Ser Leu Asp Arg Tyr Ile Lys Ile Asn Arg Ser Ile
 145 150 155 160
 Gln Gln Arg Lys Ala Ile Thr Thr Lys Gln Ser Ile Tyr Val Cys Cys
 165 170 175
 Ile Val Trp Met Leu Ala Leu Gly Gly Phe Leu Thr Met Ile Ile Leu
 180 185 190
 Thr Leu Lys Lys Gly Gly His Asn Ser Thr Met Cys Phe His Tyr Arg
 195 200 205
 Asp Lys His Asn Ala Lys Gly Glu Ala Ile Phe Asn Phe Ile Leu Val
 210 215 220
 Val Met Phe Trp Leu Ile Phe Leu Leu Ile Ile Leu Ser Tyr Ile Lys
 225 230 235 240
 Ile Gly Lys Asn Leu Leu Arg Ile Ser Lys Arg Arg Ser Lys Phe Pro
 245 250 255
 Asn Ser Gly Lys Tyr Ala Thr Thr Ala Arg Asn Ser Phe Ile Val Leu
 260 265 270
 Ile Ile Phe Thr Ile Cys Val Gly Pro Tyr His Ala Phe Arg Phe Ile
 275 280 285
 Tyr Ile Ser Ser Gln Leu Asn Val Ser Ser Cys Tyr Trp Lys Glu Ile

290	295	300
Val His Lys Thr Asn Glu Ile Met Leu Val Leu Ser Ser Phe Asn Ser		
305	310	315 320
Trp Leu Asp Pro Val Met Tyr Phe Leu Met Ser Ser Asn Ile Arg Lys		
	325	330 335
Ile Met Cys Gln Leu Leu Phe Arg Arg Phe Gln Gly Glu Pro Ser Arg		
	340	345 350
Ser Glu Ser Thr Ser Glu Phe Lys Pro Gly Tyr Ser Leu His Asp Thr		
	355	360 365
Ser Val Ala Gly Lys Ile Gln Ser Ser Ser Glu Ser Thr		
370	375	380

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 339677

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Gly Pro Arg Arg Leu Leu Leu Val Ala Ala Cys Phe Ser Leu Cys		
1	5	10 15
Gly Pro Leu Leu Ser Ala Arg Thr Arg Ala Arg Arg Pro Glu Ser Lys		
	20	25 30
Ala Thr Asn Ala Thr Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro		
	35	40 45
Asn Asp Lys Tyr Glu Pro Phe Trp Glu Asp Glu Glu Lys Asn Glu Ser		
50	55	60
Gly Leu Thr Glu Tyr Arg Leu Val Ser Ile Asn Lys Ser Ser Pro Leu		
65	70	75 80
Gln Lys Gln Leu Pro Ala Phe Ile Ser Glu Asp Ala Ser Gly Tyr Leu		
	85	90 95
Thr Ser Ser Trp Leu Thr Leu Phe Val Pro Ser Val Tyr Thr Gly Val		
	100	105 110
Phe Val Val Ser Leu Pro Leu Asn Ile Met Ala Ile Val Val Phe Ile		
115	120	125

Leu Lys Met Lys Val Lys Lys Pro Ala Val Val Tyr Met Leu His Leu
 130 135 140
 Ala Thr Ala Asp Val Leu Phe Val Ser Val Leu Pro Phe Lys Ile Ser
 145 150 155 160
 Tyr Tyr Phe Ser Gly Ser Asp Trp Gln Phe Gly Ser Glu Leu Cys Arg
 165 170 175
 Phe Val Thr Ala Ala Phe Tyr Cys Asn Met Tyr Ala Ser Ile Leu Leu
 180 185 190
 Met Thr Val Ile Ser Ile Asp Arg Phe Leu Ala Val Val Tyr Pro Met
 195 200 205
 Gln Ser Leu Ser Trp Arg Thr Leu Gly Arg Ala Ser Phe Thr Cys Leu
 210 215 220
 Ala Ile Trp Ala Leu Ala Ile Ala Gly Val Val Pro Leu Val Leu Lys
 225 230 235 240
 Glu Gln Thr Ile Gln Val Pro Gly Leu Asn Ile Thr Thr Cys His Asp
 245 250 255
 Val Leu Asn Glu Thr Leu Leu Glu Gly Tyr Tyr Ala Tyr Tyr Phe Ser
 260 265 270
 Ala Phe Ser Ala Val Phe Phe Phe Val Pro Leu Ile Ile Ser Thr Val
 275 280 285
 Cys Tyr Val Ser Ile Ile Arg Cys Leu Ser Ser Ser Ala Val Ala Asn
 290 295 300
 Arg Ser Lys Lys Ser Arg Ala Leu Phe Leu Ser Ala Ala Val Phe Cys
 305 310 315 320
 Ile Phe Ile Ile Cys Phe Gly Pro Thr Asn Val Leu Leu Ile Ala His
 325 330 335
 Tyr Ser Phe Leu Ser His Thr Ser Thr Thr Glu Ala Ala Tyr Phe Ala
 340 345 350
 Tyr Leu Leu Cys Val Cys Val Ser Ser Ile Ser Ser Cys Ile Asp Pro
 355 360 365
 Leu Ile Tyr Tyr Tyr Ala Ser Ser Glu Cys Gln Arg Tyr Val Tyr Ser
 370 375 380
 Ile Leu Cys Cys Lys Glu Ser Ser Asp Pro Ser Ser Tyr Asn Ser Ser
 385 390 395 400
 Gly Gln Leu Met Ala Ser Lys Met Asp Thr Cys Ser Ser Asn Leu Asn
 405 410 415
 Asn Ser Ile Tyr Lys Lys Leu Leu Thr
 420 425

CLAIMS

1. A purified polynucleotide encoding a polypeptide with the amino acid sequence shown in SEQ ID NO:2.

2. The polynucleotide of Claim 1 wherein the nucleic acid sequence comprises SEQ ID NO:1, or its complement.

3. A diagnostic test for conditions or diseases associated with expression of the thrombin receptor homolog (calr) in a biological sample comprising the steps of:

a) combining the biological sample with the polynucleotide of Claim 1, or a fragment thereof, under conditions suitable for the formation of hybridization complex; and

b) detecting the hybridization complex, wherein the presence of the complex correlates with expression of the polynucleotide of Claim 1 in the biological sample.

4. An expression vector comprising the polynucleotide of Claim 1.

5. A host cell transformed with the expression vector of Claim 4.

6. A method for producing a polypeptide comprising the amino acid sequence shown in SEQ ID NO:2, the method comprising the steps of:

a) culturing the host cell of Claim 5 under conditions suitable for the expression of the polypeptide; and

b) recovering the polypeptide from the host cell culture.

7. An antisense molecule comprising the nucleic acid sequence complementary to at least a portion of the polynucleotide of Claim 1.

8. A pharmaceutical composition comprising the antisense molecule of Claim 7 and a pharmaceutically acceptable excipient.

9. A method of treating a subject with a condition or disease associated with the altered expression of thrombin receptor homolog comprising administering an effective amount of the pharmaceutical composition of Claim 8 to the subject.

10. A purified polypeptide comprising the amino acid sequence of SEQ ID NO:2.

11. An agonist of the polypeptide of Claim 10.

12. A pharmaceutical composition comprising the agonist of Claim 11 and a pharmaceutically acceptable excipient.

13. A method of treating a subject with a condition or disease associated with the altered expression of thrombin receptor homolog comprising administering an effective amount of the pharmaceutical composition of Claim 12 to the subject.

14. An inhibitor of the polypeptide of Claim 10.

15. A pharmaceutical composition comprising the inhibitor of Claim 14 and a pharmaceutically acceptable excipient.

16. A method of treating a subject with a condition or disease associated with the altered expression of thrombin receptor homolog comprising administering an effective amount of the pharmaceutical composition of Claim 15 to the subject.

17. An antibody specific for purified polypeptide of Claim 10.

5 18. A diagnostic test for a condition or disease associated with the expression of the thrombin receptor homolog in a biological sample comprising the steps of:

a) combining the biological sample with the antibody of Claim 17, under conditions suitable for the antibody to bind the polypeptide and form an antibody:polypeptide complex; and

10 b) detecting the complex, wherein the presence of the complex correlates with the expression of the polypeptide in the biological sample.

19. A pharmaceutical composition comprising the antibody of Claim 17 and a pharmaceutically acceptable excipient.

20. A method of treating a subject with a condition or disease associated with the altered expression of thrombin receptor homolog comprising administering an effective amount of the pharmaceutical composition of Claim 19 to the subject.

15

5'	ATG	AGA	AGT	CAT	ACC	ATA	ACA	ATG	ACG	ACA	ACT	TCA	GTC	AGC	AGC	TGG	CCT	TAC
	Met	Arg	Ser	His	Thr	Ile	Thr	Met	Thr	Thr	Thr	Ser	Val	Ser	Ser	Trp	Pro	Tyr
	TCC	TCC	CAC	AGA	ATG	CGC	TTT	ATA	ACC	AAT	CAT	AGC	GAC	CAA	CCG	CCA	CAA	AAC
	Ser	Ser	His	Arg	Met	Arg	Phe	Ile	Thr	Asn	His	Ser	Asp	Gln	Pro	Pro	Gln	Asn
	TTC	TCA	GCA	ACA	CCA	AAT	GTT	ACT	ACC	TGT	CCC	ATG	GAT	GAA	AAA	TTG	CTA	TCT
	Phe	Ser	Ala	Thr	Pro	Asn	Val	Thr	Thr	Cys	Pro	Met	Asp	Glu	Lys	Leu	Leu	Ser
	ACT	GTG	TTA	ACC	ACA	TCC	TAC	TCT	GTT	ATT	TTC	ATC	GTG	GGA	CTG	GTT	GGG	AAC
	Thr	Val	Leu	Thr	Thr	Ser	Tyr	Ser	Val	Ile	Phe	Ile	Val	Gly	Leu	Val	Gly	Asn
	ATA	ATC	GCC	CCC	TAT	GTA	TTT	CTG	GGT	ATT	CAC	CGT	AAA	AGA	AAT	TCC	ATT	CAA
	Ile	Ile	Ala	Pro	Tyr	Val	Phe	Leu	Gly	Ile	His	Arg	Lys	Arg	Asn	Ser	Ile	Gln
	ATT	TAT	CTA	CTT	AAC	GTA	GCC	ATT	GCA	GAC	CTC	CTA	CTC	ATC	TTC	TGC	CTC	CCT
	Ile	Tyr	Leu	Leu	Asn	Val	Ala	Ile	Ala	Asp	Leu	Leu	Leu	Ile	Phe	Cys	Leu	Pro
	TTC	CGA	ATA	ATG	TAT	CAT	ATT	AAC	CAA	AAC	AAG	TGG	ACA	CTA	GGT	GTG	ATT	CTG
	Phe	Arg	Ile	Met	Tyr	His	Ile	Asn	Gln	Asn	Lys	Trp	Thr	Leu	Gly	Val	Ile	Leu
	TGC	AAG	GTT	GTG	GGA	ACA	CTG	CTT	TAT	ATG	AAC	ATG	TAC	ATT	AGC	ATT	ATT	TTG
	Cys	Lys	Val	Val	Gly	Thr	Leu	Leu	Tyr	Met	Asn	Met	Tyr	Ile	Ser	Ile	Ile	Leu
	CTT	GGA	TTC	ATC	AGT	TTG	GAT	CGC	TAT	ATA	AAA	ATT	AAT	CGG	TCT	ATA	CAG	CAA
	Leu	Gly	Phe	Ile	Ser	Leu	Asp	Arg	Tyr	Ile	Lys	Ile	Asn	Arg	Ser	Ile	Gln	Gln
	CGG	AAG	GCA	ATA	ACA	ACC	AAA	CAA	AGT	ATT	TAT	GTC	TGT	TGT	ATA	GTA	TGG	ATG
	Arg	Lys	Ala	Ile	Thr	Thr	Lys	Gln	Ser	Ile	Tyr	Val	Cys	Cys	Ile	Val	Trp	Met
	CTT	GCT	CTT	GGT	GGA	TTC	CTA	ACT	ATG	ATT	ATT	TTA	ACA	CTT	AAG	AAA	GGA	GGG
	Leu	Ala	Leu	Gly	Gly	Phe	Leu	Thr	Met	Ile	Ile	Leu	Thr	Leu	Lys	Lys	Gly	Gly
	CAT	AAT	TCC	ACA	ATG	TGT	TTC	CAT	TAC	AGA	GAT	AAG	CAT	AAC	GCA	AAA	GGA	GAA
	His	Asn	Ser	Thr	Met	Cys	Phe	His	Tyr	Arg	Asp	Lys	His	Asn	Ala	Lys	Gly	Glu

FIGURE 1A

657	666	675	684	693	702
GCC ATT TTT AAC TTC	ATT CTT GTG	GTA ATG TTC	TGG CTA ATT	TTC TTA CTA	ATA
Ala Ile Phe Asn Phe	Ile Leu Val Val	Met Phe Trp	Leu Ile Phe	Leu Leu	Ile
711	720	729	738	747	756
ATC CTT TCA TAT ATT	AAG ATT GGG	AAG AAT CTA	TTG AGG ATT	TCT AAA AGG	AGG
Ile Leu Ser Tyr Ile	Lys Ile Gly Lys	Asn Leu Leu	Arg Ile Ser	Lys Arg	Arg
765	774	783	792	801	810
TCA AAA TTT CCT AAT	TCT GGT AAA	TAT GCC ACT	ACA GCT CGT	AAC TCC TTT	ATT
Ser Lys Phe Pro Asn	Ser Gly Lys Tyr	Ala Thr Thr	Ala Arg Asn	Ser Phe	Ile
819	828	837	846	855	864
GTA CTT ATC ATT TTT	ACT ATA TGT	GTG GGT CCC	TAT CAT GCC	TTT CGA TTC	ATC
Val Leu Ile Ile Phe	Thr Ile Cys Val	Gly Pro Tyr	His Ala Phe	Arg Phe	Ile
873	882	891	900	909	918
TAC ATT TCT TCA CAG	CTA AAT GTA	TCA TCT TGC	TAC TGG AAA	GAA ATT GTT	CAC
Tyr Ile Ser Ser Gln	Leu Asn Val Ser	Ser Ser Cys Tyr	Trp Lys Glu	Ile Val	His
927	936	945	954	963	972
AAA ACC AAT GAG ATC	ATG CTG GTT	CTC TCA TCT	TTC AAT AGT	TGG TTA GAT	CCA
Lys Thr Asn Glu Ile	Met Leu Val Leu	Ser Ser Phe Asn	Ser Trp Leu	Asp Pro	
981	990	999	1008	1017	1026
GTC ATG TAT TTC CTG	ATG TCC AGT	AAC ATT CGC	AAA ATA ATG	TGC CAA CTT	CTT
Val Met Tyr Phe Leu	Met Ser Ser Asn	Ile Arg Lys Ile	Met Cys Gln	Leu Leu	
1035	1044	1053	1062	1071	1080
TTT AGA CGA TTT CAA	GGT GAA CCA	AGT AGG AGT	GAA AGC ACT	TCA GAA TTT	AAA
Phe Arg Arg Phe Gln	Gly Glu Pro Ser	Arg Ser Glu Ser	Thr Ser Glu Phe	Lys	
1089	1098	1107	1116	1125	1134
CCA GGA TAC TCC CTG	CAT GAT ACA	TCT GTG GCA	GGG AAA ATA	CAG TCT AGT	TCT
Pro Gly Tyr Ser Leu	His Asp Thr Ser	Val Ala Gly Lys	Ile Gln Ser	Ser Ser	Ser
1143					
GAA AGT ACT 3'					
Glu Ser Thr					

FIGURE 1B

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1  [M] - - - - - [M] G P R R L L L V A A C F S L C G P L L S A R T R A [R] S H T I T M T T T S V S S [S] 86700
1  [M] G P R R L L L V A A C F S L C G P L L S A R T R A [R] R P E S K A [T] N A T L D P [P] g339677

16 [W] P Y - - [S] S H R M R F I T - - - - - [N] H S D O P P Q N F S A T P N V T T C P M [M] 86700
41 [R] S F L L R N P N D K Y E P F W E D E E K N E S G L T E Y R L V S I N K S S P L [P] L g339677

49 [D] E K L - - - - - [L] S T V L T T S Y S V I F I V G L V G N [N] 86700
81 [Q] K Q L P A F I S E D A S G Y L T S S W L T L F V P S V Y T G V F V V S L P L N [N] g339677

73 [I] A P Y V F L G I H R K R N S I Q I Y L L N V A I A D L L I E C L P F R I M [M] 86700
121 [I] M A I V V F I L K M K V K K P A V V Y M L H L A T A D V L F V S V L P F K I S [S] g339677

113 [Y] H I N O N K W T L G V I L C K V V G T L L Y M N M Y I S I L L G F I S L D R [R] 86700
161 [Y] Y F S G S D W Q F G S E L C R F V T A A F Y C N M Y A S I L L M T V I S I D R [R] g339677

153 [Y] I K I N R S I Q O R K A I T T K O S I Y V C C I V W M L A L G G F L T M I I - [I] 86700
201 [F] L A V V Y P M Q S L S W R T L G R A S F T C L A I W A L A I A G V V P L V L K [K] g339677

192 [L] T L K K G G H N S T M C F H Y R D K H N A K G E A I F N F - - [I] L V V M F W [W] 86700
241 [E] Q T I Q V P G L N I T T C H D V L N E T L L E G Y Y A Y Y F S A F S A V F F [F] g339677

229 [L] I F L L I I L S Y I K I G K N L L R - - [I] S K R R S K F P N S G K Y A T T A R [R] 86700
281 [V] P L I I S T V C Y V S I I R C L S S S A V A N R S K K - - S R A L F L S A A - [A] g339677

267 [N] S F I V L I I F T I C V G P Y H A F - - [R] F I Y I S S Q L N V S S C Y W K E [E] 86700
318 [V] F C I E I I C F G P T N V L L I A H Y S F L S H T S T T E A A Y F A Y [Y] g339677

304 [I] V H K T N E I M L V L S S F N S W L D P V M Y F L M S S N I R K I M C O L L F [F] 86700
354 [L] L C - - - - - V C V S I S I S C I D P L I Y Y A S S E C Q R Y V Y S I L C [C] g339677

344 [R] R F O G E P S R S E S T S E F K P G Y S L H D T S V A G K I O S S S E S T [T] 86700
388 [C] K E S S D P S S Y N S S G Q L M A S K M D T C S S N L N N S I Y K K L L T [T] g339677

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FIGURE 2



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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C12Q 1/68, C12N 5/10, A61K 48/00,
38/17, G01N 33/50

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US

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(81) Designated States: AL, AM, AT, AU, AZ, BB, BG, BR, BY,
CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL,
IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV,
MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU,
SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, UZ, VN,
ARIPO patent (KE, LS, MW, SD, SZ, UG), Eurasian patent
(AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent
(AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU,
MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM,
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(57) Abstract

The present invention provides nucleotide and amino acid sequences that identify and encode a novel thrombin receptor homolog (TRH) expressed in human liver. The present invention also provides for antisense molecules to the nucleotide sequences which encode TRH, diagnostic tests based on TRH encoding nucleic acid molecules, expression vectors for the production of purified TRH, antibodies capable of binding to TRH, hybridization probes or oligonucleotides for the detection of TRH-encoding nucleotide sequences, genetically engineered host cells for the expression of TRH, and antagonists, antibodies and inhibitors which bind to the polypeptide TRH.

1' 2' 3' 4' 5' 6' 7' 8' 9' 10' 11' 12' 13' 14' 15' 16' 17' 18' 19' 20' 21' 22' 23' 24' 25' 26' 27' 28' 29' 30' 31' 32' 33' 34' 35' 36' 37' 38' 39' 40' 41' 42' 43' 44' 45' 46' 47' 48' 49' 50' 51' 52' 53' 54' 55' 56' 57' 58' 59' 60' 61' 62' 63' 64' 65' 66' 67' 68' 69' 70' 71' 72' 73' 74' 75' 76' 77' 78' 79' 80' 81' 82' 83' 84' 85' 86' 87' 88' 89' 90' 91' 92' 93' 94' 95' 96' 97' 98' 99' 100' 101' 102' 103' 104' 105' 106' 107' 108' 109' 110' 111' 112' 113' 114' 115' 116' 117' 118' 119' 120' 121' 122' 123' 124' 125' 126' 127' 128' 129' 130' 131' 132' 133' 134' 135' 136' 137' 138' 139' 140' 141' 142' 143' 144' 145' 146' 147' 148' 149' 150' 151' 152' 153' 154' 155' 156' 157' 158' 159' 160' 161' 162' 163' 164' 165' 166' 167' 168' 169' 170' 171' 172' 173' 174' 175' 176' 177' 178' 179' 180' 181' 182' 183' 184' 185' 186' 187' 188' 189' 190' 191' 192' 193' 194' 195' 196' 197' 198' 199' 200' 201' 202' 203' 204' 205' 206' 207' 208' 209' 210' 211' 212' 213' 214' 215' 216' 217' 218' 219' 220' 221' 222' 223' 224' 225' 226' 227' 228' 229' 230' 231' 232' 233' 234' 235' 236' 237' 238' 239' 240' 241' 242' 243' 244' 245' 246' 247' 248' 249' 250' 251' 252' 253' 254' 255' 256' 257' 258' 259' 260' 261' 262' 263' 264' 265' 266' 267' 268' 269' 270' 271' 272' 273' 274' 275' 276' 277' 278' 279' 280' 281' 282' 283' 284' 285' 286' 287' 288' 289' 290' 291' 292' 293' 294' 295' 296' 297' 298' 299' 300' 301' 302' 303' 304' 305' 306' 307' 308' 309' 310' 311' 312' 313' 314' 315' 316' 317' 318' 319' 320' 321' 322' 323' 324' 325' 326' 327' 328' 329' 330' 331' 332' 333' 334' 335' 336' 337' 338' 339' 340' 341' 342' 343' 344' 345' 346' 347' 348' 349' 350' 351' 352' 353' 354' 355' 356' 357' 358' 359' 360' 361' 362' 363' 364' 365' 366' 367' 368' 369' 370' 371' 372' 373' 374' 375' 376' 377' 378' 379' 380' 381' 382' 383' 384' 385' 386' 387' 388' 389' 390' 391' 392' 393' 394' 395' 396' 397' 398' 399' 400' 401' 402' 403' 404' 405' 406' 407' 408' 409' 410' 411' 412' 413' 414' 415' 416' 417' 418' 419' 420' 421' 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GA	Gabon			VN	Viet Nam

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/12 C12N15/11 C07K14/705 C12Q1/68 C12N5/10
 A61K48/00 A61K38/17 G01N33/50

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C07K A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO,A,92 14750 (UNIV CALIFORNIA ;COR THERAPEUTICS INC (US)) 3 September 1992 see the whole document ---	11-13
A	EMBL EST, Accession no R71586, Sequence reference yi52d09.r1, 03-jun-1995, Homo sapiens cDNA clone 142865 5'. XP002018616 see the whole document ---	1
A	WO,A,94 12635 (ICOS CORP) 9 June 1994 sequence no 44 ---	1
P,X	US,A,5 516 889 (HOLLENBERG MORLEY D ET AL) 14 May 1996 see the whole document ---	11-13
	-/--	



Further documents are listed in the continuation of box C.



Patent family members are listed in annex.

* Special categories of cited documents :

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- "O" document referring to an oral disclosure, use, exhibition or other means
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"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

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"&" document member of the same patent family

Date of the actual completion of the international search

15 November 1996

Date of mailing of the international search report

22. 11. 96

Name and mailing address of the ISA

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Authorized officer

Chambonnet, F

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 96/08948

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,A	EP,A,0 672 757 (BASF AG) 20 September 1995 see the whole document -----	14-16

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 96/08948

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
Remark: Although claim(s) 9, 13, 16 and 20
is(are) directed to a method of treatment of the human/animal
body, the search has been carried out and based on the alleged
effects of the compound/composition.
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such
an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all
searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment
of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report
covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is
restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 96/08948

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
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